

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 07:03:59 ; Search time 28.35 Seconds

(without alignments)

699.671 Million cell updates/sec

Title: US-09-652-292-2

Perfect score: 2765

Sequence: 1 MGHSPVPLPCASVSLGGL.....CHRONSTGTPYSRIEISAAS 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	21.4	461	1 CSBC_BACSU	P46333 bacillus su
2	571	20.7	457	1 XLT_LACBR	O52733 lactobacill
3	520.5	18.8	557	1 ITR2_SCHPO	P87110 schizosacch
4	499	18.0	464	1 GALP_ECOLI	P37021 escherichia
5	497.5	18.0	547	1 GTR1_LEIDO	Q01440 leishmania
6	495	17.9	472	1 ARAE_ECOLI	P09830 escherichia
7	489.5	17.7	472	1 ARAE_KLEOX	P45598 klebsiella
8	484.5	17.5	522	1 ITR1_ARATH	P23586 arabidopsis
9	473.5	17.1	575	1 ITR1_SCHPO	Q10286 schizosacch
10	467	16.9	523	1 STC_RICCO	Q41144 ricinus com
11	464.5	16.8	468	1 GLCP_SYNY3	P15729 synechocyst
12	460	16.6	491	1 XYLE_ECOLI	P09098 escherichia
13	452.5	16.4	482	1 YFIG_BACSU	P54723 bacillus su
14	438	15.8	584	1 ITR1_YEAST	P30605 saccharomyc
15	430.5	15.6	522	1 STA_RICCO	Q10710 ricinus com
16	418.5	15.1	522	1 GTR2_RAT	P12336 rattus norv
17	409	14.8	612	1 ITR2_YEAST	P30606 saccharomyc
18	408.5	14.8	473	1 GLF_ZYMMO	P21906 zymomonas m
19	407.5	14.7	509	1 GTR4_HUMAN	P14672 homo saplen
20	405.5	14.7	495	1 GTR3_CANFA	P47842 canis famli
21	405	14.6	510	1 GTR4_MOUSE	P14142 mus musculu
22	404.5	14.6	494	1 GTR3_SHEEP	P47843 ovis aries
23	403	14.6	523	1 GTR2_MOUSE	P14246 mus musculu
24	401.5	14.5	509	1 GTR4_RAT	P19357 rattus norv
25	399	14.4	763	1 RGT2_YEAST	Q12300 saccharomyc
26	397	14.4	546	1 HXT0_YEAST	P43581 saccharomyc
27	396	14.3	510	1 HEX6_RICCO	Q07423 ricinus com
28	396	14.3	567	1 RAG1_KLULA	P18631 kluyveromyc
29	395.5	14.3	540	1 HUP2_CHLKE	Q39524 chlrella k
30	394.5	14.3	496	1 GTR3_CHICK	P28568 gallus gall
31	394.5	14.3	524	1 GTR2_HUMAN	P11168 homo saplen
32	392.5	14.2	534	1 HUP1_CHLKE	P15686 chlrella k
33	390	14.1	541	1 HAT2_YEAST	P23585 saccharomyc

34	388	14.0	533	1 GTR2_CHICK	Q90592 gallus gall
35	387	14.0	534	1 HUP3_CHLKE	Q39525 chlrella k
36	383.5	13.9	490	1 GTR1_CHICK	P46896 gallus gall
37	381	13.8	551	1 HGT1_KLULA	P49374 kluyveromyc
38	381	13.8	594	1 RCO3_NEUCR	Q92253 neurospora
39	379.5	13.7	496	1 GTR3_HUMAN	P11169 homo saplen
40	378.5	13.7	493	1 GTR3_MOUSE	P32037 mus musculu
41	376.5	13.6	493	1 GTR3_RAT	Q07647 rattus norv
42	375.5	13.6	492	1 GTR1_HUMAN	P11166 homo saplen
43	375.5	13.6	566	1 KHT2_KLULA	P53387 kluyveromyc
44	374.5	13.5	492	1 GTR1_BOVIN	P27674 bos taurus
45	374.5	13.5	592	1 HXT5_YEAST	P38695 saccharomyc

ALIGNMENTS

RESULT 1

CSBC_BACSU STANDARD; PRT; 461 AA.
ID P46333; O32289;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE METABOLITE TRANSPORT PROTEIN CSBC.
GN CSBC OR SS92BR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=96093926; PubMed=7584049;
RA Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
RT "Cloning and sequencing of a 36-kb region of the Bacillus subtilis
genome between the gnt and lol operons.";
RL DNA Res. 2:61-69(1995).
RN [2]
RP REVISIONS.
RA Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.-I.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99303315; PubMed=10376822;
RA Akbar S., Lee S.Y., Boylan S.A., Price C.W.;
RT "Two genes from Bacillus subtilis under the sole control of the
general stress transcription factor sigmaB.";
RL Microbiology 145:1069-1078(1999).
CC -!- FUNCTION: COULD SERVE EITHER A NUTRITIONAL OR AN OSMOTIC
PROTECTION FUNCTION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB005554; BAA21604.1; -;
DR EMBL; Z99124; CAB16017.1; -;
DR Subtilist; BG11360; csbc.
DR InterPro; IPR003663; Sugar_transpstr.
DR InterPro; IPR003662; sub_transpstr.
DR Pfam; PF00083; sugar_tr; 1.

```

17 LGGLTFGYELAVISGALLPLQLDGLSCLEQEFVLGSLLLGALLASLVGGFLIDCYGRKQ 76
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 LGGFLFCYDGTGVISGAILFIQKQNNLGSWQGVWSAVLLGAILGAILGAIQPSDRGGRK 74
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 AILGSNLVLIAGSLUTGLIAGSLAWLVUGRAVYFAISLSMACCIYSEIVLGPQRGVLV 136
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 LLLLSAIIFFVAGLSAFSPFEWTLIISRIILGMVAGSASALIPTVLAELAPSDKRGTVS 134
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 SLYEAGITVTVGLLSYALNYALACTPCWGRIMFGWATAPAVLOSLSLLFLPAGT- 189
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 SLFOLMVTGTILLAYITNYSFGYITGWRWMLGFAIPAALLFGLLIUFPESPRFLVKS 194
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
190 -----DETATHKDLIPLQCGEAPKLGPRPRYSFLDLFRADNMGRGTV 234
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
195 HLDEARHVLDTMKNHQVAVNKEINDIQ--ESAKIVSG----GWSELFGEKM--VRSLLII 246
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 GLGLVLFOOQTGPQNVLCYASTITSSVFGFHGGSASVLASVGLGAVKVAATLTAMGLVDRA 294
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 GIGLAIPOQWYMGNTVLYAPTFTDVG- GVSAAALLAHIGIGFNVIIVTAIAVIMDKI 305
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
295 GRALLLAGCALMALNSVGIGLVSFAPVPMDSGPSCLAVPNATQOTGLPGDGLQDSSLP 354
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 DRKKNIGAVMGIS---LFVMSIGMKFSGQSOTAAI----- 340
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
355 PIPTNEDQREPIILSTAKTKPHPRSGDPSAPPRLASSALPGPLPARGHALLRWTA 414
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
341 -----ISVI 344
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415 CLMVFSAFSGFGPVTWLVLSIYVPEIKGRAFCNSFNMAANLFISSLFDLIGTIG 474
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

QY      235  GLGLVLFQOQLTGQPNVLCASTTFSSVFHGGSSAVLASVGLGAVKVAATLTAMGLVDRA 294
         | : | : | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db      247  GIGLAIFQQVMGNTVLYAPTFTDVG- GVSAALLAHITGIFNVIVTALAVALMDKI 305
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      295  GRALLAGCALMALNSVSGTGLVSEFAPMDSGFSCLAVPNATQTGLPGDSLGLLDSSLP 354
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      306  DRKKIYNIGAVMGIS---L FVMSIGMKFGSGQTAAI----- 340
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      355  PIPRTNEDQREPIILSTA KTKPHPRSGDSPAPRLALSSALPGPLPARGHALLRWTALL 414
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      341  -----ISVI 344
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      415  CLMVFSARSGFGPPVTWLVSIIYPVEIKGRAFCNSFNMAANFLISLSFDLDLIGTIG 474
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Db 345 ALTYYIAFFSATGPMVMWIGEVPLNIRGLGNFSFASVINWNTANMIYLSLTFPSLLDFG 404

Qy 475 LSWTFLLYGLVFLGLGFIYLVFVETKQSLAEID 509

Db 405 TGSFLFIGYGLCFASIMPVQKKVFPETNRNLSLEDIE 439

RESULT 3

ID ITR2_SCHPO STANDARD; PRT; 557 AA.

AC P87110; P78901;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE MYO-INOSITOL TRANSPORTER 2.

GN ITR2 OR SPAC20G8.03.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=968 H90;

RX MEDLINE=96228265; PubMed=9560432;

RA Niederberger C., Graub R., Schweingruber A.-M., Fankhauser H.,

Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.;

RT "Exogenous inositol and genes responsible for inositol transport are

required for mating and sporulation in *Schizosaccharomyces pombe*.";

RL Curr. Genet. 33:255-261(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 166-541 FROM N.A.

RC STRAIN=PR745;

RA Yoshioka S., Kato K., Okayama H.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TRANSPORTER FOR MYO-INOSITOL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X99105; ; NOT ANNOTATED_CDS.

DR EMBL; Z95334; CAB08597.1; ;

DR EMBL; D89252; BAA13913.1; ;

DR InterPro; IPR003663; Sugar_trnsportr.

DR InterPro; IPR003662; sub_trnsportr.

DR Pfam; PF00083; sugar_tr; 1.

DR PRINTS; PR00171; SUGCTRNSPORT.

DR PRINTS; PR00172; GLUCTRNSPORT.

DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.

DR PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.

DR KW Transmembrane; Sugar transport; Glycoprotein.

FT TRANSMEM 77 97 POTENTIAL.

FT TRANSMEM 100 120 POTENTIAL.

FT TRANSMEM 124 144 POTENTIAL.

FT TRANSMEM 158 178 POTENTIAL.

FT TRANSMEM 181 201 POTENTIAL.

FT TRANSMEM 210 230 POTENTIAL.

FT TRANSMEM 241 261 POTENTIAL.

FT TRANSMEM 368 388 POTENTIAL.

FT TRANSMEM 397 417 POTENTIAL.

FT TRANSMEM 433 453 POTENTIAL.

FT TRANSMEM 469 489 POTENTIAL.
FT TRANSMEM 499 519 POTENTIAL.
FT DOMAIN 520 557 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 271 271 N -> H (IN STRAIN PR745).
FT VARIANT 428 428 N -> H (IN STRAIN PR745).
FT VARIANT 436 436 L -> I (IN STRAIN PR745).
FT VARIANT 526 526 S -> F (IN STRAIN PR745).
SQ SEQUENCE 557 AA; 61136 MW; 20875EC1B153175 CRC64;

Query Match 18.8%; Score 520.5; DB 1; Length 557;
Best Local Similarity 27.1%; Pred. No. 1.8e-25;
Matches 144; Conservative 90; Mismatches 189; Indels 109; Gaps 10;

Qy 12 ASVSLGLTFGYELAVISGALLPLQDFG--LSCQEFLVGSLLGLGALLASLVGGPLI 69

Db 85 SAVAGISGLLFGYDTGVISGALAVLGSDLGHVLSGGQKELITSATSPAALISATTSGWLA 144

Qy 70 DCYGRKQAILGSNLVLAGSLTGLAGSLAWLVGVAVGVPAISLSSMACCIYVSELVGP 129

Db 145 DWGRKRLLLCADAIFVIGSVIMAAARNVAMVVGRTFVGVGIGLTSLVPMYITELAPA 204

Qy 130 RQGVLSLYEAGITVGILLSYALNYALAGTPGWRHMFHGNATAPAVLOSLSLLPLPAGT 189

Db 205 RLGRGLVYIVYFTGGQLIAYSLNAAFEHVHQQWRIMFGIGAAPALGQLISLFWTPEP 264

Qy 190 DETATH---KDLIPLOGGEAPKLGPRDPRY-----SFLDLF 222

Db 265 RYLLRHNVKVVYKILSRHPEAKPAETAYKVSLOEGVKVDFPEGNKQFHHFSLKVLFP 324

Qy 223 RARDNRGRTTVGLGLVLFQQLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKA 282

Db 325 TVPSNRRS-LFTGCFLOWFQFSGTNAIQYFSAITFQSGF---KNSISVSVVVGATNFV 380

Qy 283 ATLTAMGLVDRAGRRALLLAGCALMALSVSGVLGVSPAVPMDSGSPCLAVPNATQGTGLP 342

Db 381 FTIVAFMFIDRIGRRRILLCTSAVM---IAGLALCAIAYHF-----LP 420

Qy 343 GDSGLLDLSDLPPIPTNEDQREPISTAKTKPKHPRSGDPSAPPRLALSALPGPLPA 402

Db 421 AD-----TQNTNSG----- 430

Qy 403 RGHALLRTWALLCMVVSASFSGFGPVTVLVSIIYVEIRGRAFCNFSNNAANLFI 462

Db 431 -----WQYVVLASIIIFLASVAGSINGIPW-QQAEFLPMNEVRALCAGFSTAINMWGNLI 484

Qy 463 SLFLDLTGTLGSLTWTFLLYGLTAVLGLGFIYLVFVETKQSLAEIDQFOF 514

Db 485 SASPLTMMESITPTGTFTALFAGFCFVGLVTSTYFTYPELAGMSIENIKLLEK 536

RESULT 4

GALP_ECOLI

ID GALP_ECOLI STANDARD; PRT; 464 AA.

AC P37021;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE GALACTOSE-PROTON SYMPORTER (GALACTOSE TRANSPORTER).

GN GALP OR B2943.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RA Roberts P.E.;

RL Thesis (1992), University of Cambridge, U.K.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

```

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT *The complete genome sequence of Escherichia coli K-12.*;
RL Science 277:1453-1474(1997).
CC -!- FUNCTION: UPTAKE OF GALACTOSE ACROSS THE BOUNDARY MEMBRANE WITH
CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U28377; AAA69110.1; -.
DR EMBL; AE000377; AAC75980.1; -.
DR EcoGene; EG12148; galP.
DR InterPro; IPR003663; Sugar_trnsportr.
DR InterPro; IPR003662; sub_trnsportr.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
KW Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 85 105 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 140 160 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 395 415 POTENTIAL.
FT TRANSMEM 417 437 POTENTIAL.
SQ SEQUENCE 464 AA; 50982 MW; 07E08935BD8E3F8E CRC64;

Query Match      18.0%; Score 499; DB 1; Length 464;
Best Local Similarity 27.2%; Pred. No. 3.2e-24;
Matches 141; Conservative 95; Mismatches 183; Indels 100; Gaps 10;

QY   14  VSLLGGITFCGYELAVISGALLPLQLDFGLSCLEBOFLVGLSLLGALLASIVSGFLDCVG 73
Db    : : | | | | : : | | | | : : : : | | | | : : : : | | : |
Dy   21  LAALAGLLFGDLIGVTAGALPFITAEDEFQTTSQEWVSSMMFMGAAGVAVGSGWLSFKLG 80
DY    : : | | | | : : | | | | : : | | : : | | : : | | : |
QY   74  RKQAILGSNLVLVLAGSLITGLAGSLAWLVGRAVVGFALSLSMACCIIYVSSELVGROR 133
Db    : : | | | | : : | | | | : : | | : : | | : : | | : |
Dy   81  RKKSLMGAILFVAGSLFSAAAPNVEVILLSRVLGLAVGVASYTAPLYLSIAPEKING 140
DY    : : | | | | : : | | | | : : | | : : | | : : | | : |
QY   134 VLVSLEYAGITVGIILSYALNALAGTPGWGRHMFQWATAPAVLOSLSLFLFPACGTDETA 193
Db    ::::| | : | | | : : | | : : | | : : | | : : | | : |
Dy   141 SMISYQLMTIIGILGAYLSDTAFSYT-GAWRMLCVIIIPAILLLIGVFVLPDSPRPFA 199
DY    : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   194 THKDLDLPLO-----GGEAPK-LGCRP----RYSELDLFRARDNNRGTTTVGLGLIV 239
Db    : : : : : : | | : | : : | : : | : : | : : | : : |
Dy   200 AKRRFYDAERVLLRLRDTSAEKRELDLETRESLQVKQSGWALFKENSFRFAVFI LGVLLQ 259
DY    : : : : : : | | : | : : | : : | : : | : : | : : |
QY   240 LFOQLTGOPNVLCYASTIFESSVGFHGGSAAVLASVGLGAVKVAATLTAMGLVDRAGRAL 299
Db    : : | | : : | | : : : : : : : : : : : : | | : | : |
Dy   260 VMQQFTGMNVIMVYAPKIFELAGYTNTTFQMWGTVIVGLTNVLAFTFIALGLVDRNGRPT 319
DY    : : | | : : | | : : : : : : : : : : : : | | : | : |
QY   300 LLAGCALMALSVSGIGLCLVSPVMDSGPSCLAVPNATGQTGLPGDSGLLQDSSLPIIPT 359
Db    : : | | : : | | : : : : : : : : : : : : | | : | : |
Dy   320 LTGLGLVMA---AGMCVLG-----
DY    : : | | : : | | : : : : : : : : : : : : | | : | : |

```

```
Db 7 LCAG---LGGFLGDTGTVINAALFQMKDFGFEHSHSQYALIVAIATAGAFVGSF 63
Qy 68 LIDCYGRKQAILGNLLVLAGSLAGSLAVLGRVAVGFAISLSSMACCIYVSELV 127
Db 64 ISAAFGRRPCIAVADALFVIGSVLMGAAPNVEVLVSRVIVGLAIGISSATIPYLAET 123
Qy 128 GPRGCVLSYIYAGITVIGILLS---YALNYALAGTGMWRHMFGMTAPAVLSLSLLF 184
Db 124 SPKRGATIVLNNFLFTGGQFVAAGFTAIMVFTSKNIGRVAIGIGALPAVVOAFCLLF 183
Qy 185 -----LPAGTDEAT-----HKDLIPLO-CGGEAPKLGPRPRYSFLDLFRARDNM 228
Db 184 FLPSRWLLSKGHADRAKAVADRFEDLCEFOEGDELPSV-----RIDYRPLM-ARD-M 236
Qy 229 RGRTVGLGLVLFQOLTQOPNVLCYASTFSSVGFHGGSSAVLASVIGAVKVAATLTAM 288
Db 237 RFRVVLSSGLQIQOFSGINTIYSSVILYDAGFRDAIMPVLSIPLAFNNALFTAVAI 296
Qy 289 GLVDRAGRALLLA---GCALMALSVSGIGL-----VSFAVPMDSGSPCLAVPNATGOTG 340
Db 297 FTVDFFRRRRLLSVFGCLLVVIAIIGFICTRISYSV----- 337
Qy 341 LPDGSGLQDSSLPPIPTNEDQREPILSAKTKPKHPRSGDPSAPPRALSSALPGPPL 400
Db 338 ---CGGLF----- 342
Qy 401 PARGHALLRWTALECLMVFVSFAFGFQPVVWLVLSEIYVEIRGAFACNCFNNAANL 460
Db 343 -----LALLAVFLALYAPGICIPWVINGEIPFHLRTSAASVATMANWGANV 390
Qy 461 FISLFDLIGTIGLWTFLLYGLTAVLGLGFIYFLVPETKQSLAEIDQOQFRK----- 515
Db 391 LVSVFFILMGAIVGGTFTIISGLMALGCIFFVFFAVETKGLTLEQIDNNFRKRLGPP 450
Qy 516 RFTLSFGHRSNTG 529
Db 451 RF-----HEEGSG 459

RESULT 6
ARAE_ECOLI STANDARD; PRT; 472 AA.
AC P09830; Q46937;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ARABINOSE-PROTON SYMPORTER (ARABINOSE TRANSPORTER).
GN ARAE OR B2841 OR Z4161 OR ECS3698.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87115869; PubMed=3543693;
RA Maiden M.C.J., Jones-Nortimer M.C., Henderson P.J.F.;
RA Henderson P.J.F.;
RT "Mammalian and bacterial sugar transport proteins are homologous.";
RL Nature 325:641-643(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / JM2433;
RX MEDLINE=88228015; PubMed=2836407;
RA Maiden M.C.J., Jones-Nortimer M.C., Henderson P.J.F.;
RT "The cloning, DNA sequence, and overexpression of the gene araE
coding for arabinose-proton symport in Escherichia coli K12.";
RL J. Biol. Chem. 263:8003-8010(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
```

```
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregory J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potanousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 050952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Ikeda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RP PRELIMINARY SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=84114868; PubMed=6319708;
RA Stoner C., Schleich R.F.;
RT "The araE low affinity L-arabinose transport promoter. Cloning,
sequence, transcription start site and DNA binding sites of
regulatory proteins.";
RL J. Mol. Biol. 171:369-381(1983).
CC -1- FUNCTION: UPTAKE OF ARABINOSE ACROSS THE BOUNDARY MEMBRANE WITH
THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed, usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
EMBL; J03732; AAA23469.1; -
DR EMBL; X00272; CAA25075.1; -
DR EMBL; U29581; AAB40488.1; -
DR EMBL; AE000368; AAC75880.1; -
DR EMBL; AE005513; AAC75853.1; -
DR EMBL; AP002563; BAB37121.1; -
DR PIR; B26430; B26430.
DR PIR; A28075; A28075.
DR EcoGene; EG10056; araE.
DR InterPro; IPR003663; Sugar_transprt.
DR InterPro; IPR003662; sub_transprt.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
Complete proteome.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 92 110 POTENTIAL.
FT TRANSMEM 120 138 POTENTIAL.
FT TRANSMEM 149 167 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
```



```

Db 357 -LSWLSVGNMNCIAGYAMSAAPVWVWILCSEIQLKCRDFGTCSTTTNWNWMIIGATF 415
QY 467 LDLICTIGLWTFYLYGLTAVLGLGFIYLVFPETKGSLAEIDQO 511
Db 416 LTLDAIGAAGTFWLYTALNVAFIGVTFWLPETKRVNLTIEHRR 460

RESULT 8
STPL_ARATH
ID STPL_ARATH STANDARD; PRT; 522 AA.
AC P23586;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GLUCOSE TRANSPORTER (SUGAR CARRIER).
GN STPL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERECTA;
RX MEDLINE=9100595; PubMed=2209537;
RA Sauer N., Friedlaender K., Graeml-Wicke U.;
RT Primary structure, genomic organization and heterologous expression
RT of a glucose transporter from Arabidopsis thaliana.;
RL EMOB J. 9:3045-3050(1990).
CC -1- FUNCTION: ACTIVE UPTAKE OF HEXOSES. PROBABLE GLUCOSE/HYDROGEN
CC SYMPORT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55350; CAA39037.1; .
DR PIR; S12042; S12042.
DR InterPro; IPR003663; Sugar_trnsportr.
DR InterPro; IPR003662; sub_trnsportr.
DR Pfam; PF00083; sugar_tr.1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PRINTS; PR00172; GLUCTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane; Transport; Sugar transport; Symport.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 321 341 POTENTIAL.
FT TRANSMEM 349 369 POTENTIAL.
FT TRANSMEM 385 405 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 453 473 POTENTIAL.
FT DOMAIN 474 522 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 522 AA; 57596 MW; 68A6C72A6FFD90380 CRC64;

Query Match 17.5%; Score 484.5; DB 1; Length 522;
Best Local Similarity 26.0%; Pred. No. 2.9e-23;
Matches 154; Conservative 96; Mismatches 183; Indels 159; Gaps 17;

```

```

QY 4 SPPVPLCASVSLGLTGFYELAVISGAL-LP---LQLDLGLSLCEOE----- 48
Db 20 TPFVFLTCV-VAAMGGLIFGVDIGISGGVTSMPSEKRFPSVYRQKQEDASTNQYCYQVD 78
QY 49 -----FLVGSLLGLALLASLGGFLIDCYGRKQATLGSNLVLLAGSLTGLAGSLAWLVL 103
Db 79 SPTLTMTFTSSLYLAALISLVASTVTRKGRRLSLMFLGGLFCACALINGFAKHVWMLIV 138
QY 104 GRVYVGFPAISLSSMACCIYVSELVGRGVRVLSIYEAGITVIGILLSTALNYALAGTP--- 161
Db 139 GRILLGFGIGFANQAVPLYLSEMAPYKYRGALNIGFQLSITIGILVAEVLNFFAKIRGG 198
QY 162 WGRHMFQWATAPAVLQSLSLFLP-----AGTDTATHKDLI 199
Db 199 WGRULSLGAVVPALIIITIGISLVLPDTPNSMIERQHEAKTKLRIRGVDDVSQEFDDL 258
QY 200 PLOGGEAPKLGPRDRYSFLDLFRARDNMGRRTTVGLGLVLFQOOLTGPVNLVLCYASTIFS 259
Db 259 VAASKESQSI-----EHPWRNLLRRK--YRPHLTMAVMIPFPQOLTGINVIFYAPVLFN 311
QY 260 SVGFHGGSSAVLASVGLGAVKVAATLTAMGLVDRAGRALLAGCALMALSVSGIGLVSF 319
Db 312 TIGFTTDDAS-LMSAVVTGVSNNVGATLVSIYGVDRGRFRFLFLEGGTOMLI----- 360
QY 320 AVPMDSGSPCLAVPNAT-----GQTGLPGDSCLLQDSSLPPIPTNEDOREPILSTAKKT 374
Db 361 -----CQAVVAACIGAKFGVDGTPGE----- 381
QY 375 KPHRSRGPSPAPPRIALSSALPGPPLPARGHALLRWLTALLC---LMVFVSAPSFSGFPVT 431
Db 382 -----LPKWAIVVVVTFICIVVAGFANSGPLG 409
QY 432 WLVLSEIYPVEIRGRAFCNSFNWAANLFLSLFLDLIGTI--GLSWTFLLYGLTAVLG 489
Db 410 WLVPSEIPLFIRSAAQSITVSNNMIFITIAQLFELMLCHLKLEGL---FLVFAFVVVM 466
QY 490 LGFIYLVPEYKQSLAEIDQOQFQR-----RF-----TLSFGRHNSGTG 529
Db 467 SIFVYIFLPETKGIPEEMGOVWRSHWYSRFEVDGEYGNALMGKNSNQAG 518

RESULT 9
ITRL_SCHPO
ID ITRL_SCHPO STANDARD; PRT; 575 AA.
AC Q10286;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYO-INOSITOL TRANSPORTER 1.
GN ITRI OR SPAC7D4.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968 H90;
RX MEDLINE=98228265; PubMed=9560432;
RA Niederberger C., Graub R., Schweingruber A.-M., Fankhauser H.,
RA Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.;
RT Exogenous inositol and genes responsible for inositol transport are
RT required for mating and sporulation in Schizosaccharomyces pombe.;
RL Curr. Genet. 33:255-261(1998).
RN [2]
RP SEQUENCE OF 290-575 FROM N.A.
RC STRAIN=972;
RA Gentles S., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSPORTER FOR MYO-INOSITOL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----

```

QY	449	ATCNSFNNAANFLISLSFLDLIGTIGLWTFLLYGLTAVLG-LGFIYLFVPETKGSLAE	507
Db	481	GMSTAVNNAAGNIGCASELTLMSEITPTGFALYGLGLGALFCY-PDLTDYIEE	539
QY	508	IDQQFKRRFTLSFGHON	526
Db	540	IGELLKH-----GFGVRES	553

```

DB      540 IGELLKH-----GFGVRES 553

RESULT 10
STC_RICCO
ID      STC_RICCO      STANDARD;      PRT;      523 AA.
AC      Q41144; Q41147;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      SUGAR CARRIER PROTEIN C.
STC.
OS      Ricinus communis (Castor bean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eustosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX      NCBI_TaxID=3988;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. CARMENCITA; TISSUE=Cotyledon;
RA      Weig A., Franz J., Sauer N., Komor E.;
RT      "Isolation of a family of cDNA-clones from Ricinus communis L.
RT      with close homology to the hexose carriers.";
RRL      J. Plant Physiol. 143:178-183(1994).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC      -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

```

----- Send an email to license@isd-sid.ch) -----
EMBL; L08196; AAA79761.1; -
EMBL; L08191; AAA79764.1; -
InterPro; IPR003663; Sugar_transportr.
InterPro; IPR003662; sub.transprot.
Pfam; PF00083; sugar.tr. 1.
PRINTS; PR00171; SUGETRNSPORT.
PRINTS; PR00172; GLUCTRNSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Transport; Sugar transport; Symport.
TRANSMEM   25    45    POTENTIAL.
TRANSMEM      85   105    POTENTIAL.
TRANSMEM     120   140    POTENTIAL.
TRANSMEM     143   163    POTENTIAL.
TRANSMEM     205   225    POTENTIAL.
TRANSMEM     298   318    POTENTIAL.
TRANSMEM     341   341    POTENTIAL.
TRANSMEM     351   371    POTENTIAL.
TRANSMEM     387   407    POTENTIAL.
TRANSMEM     430   450    POTENTIAL.
TRANSMEM     455   475    POTENTIAL.
Q SEQUENCE 523 AA; 57769 MW; 074804EFA3A27F6B CRC64;

Query Match              16.9%; Score 467; DB 1; Length 523;
Best Local Similarity    26.2%; Pred. No. 3.5e-22;
Matches 148; Conservative 91; Mismatches 161; Indels 164; Gaps 16;

Y 14 VSLGLGTFGYELAVISCALLPLQLDFGLSCLEOF-----SPKFFGRVSVVVVFVAAGNGNCCGCCTC
b 31 VAAMGGLLFGYGDIG-IGSGVMSP-----SPIKKFRGVVVVVVFVAAGNGNCCGCCTC-----

```



```

Qy 50 --LVGSLLLGALLASLVCGFLIDCYGRKQAILGSLNVLVLAGSLTGLAGSLANVLVGRV 107
Db 85 TMTSSLYLAALIASLVASTITRFGKRLSMLFGVLCFAGAIINGAAKAYMMLTGLRIL 144
Qy 108 VGFATLSGSMACCIIVSELVGRGVLSVLEAGITVIGLLSVNALVALAGTP--WGWR 165
Db 145 LQFGIGFANOSVPLVSEMAPYKRGALNIGFQISITIGILVANVLYFFAKIKGGWGR 204
Qy 166 HMFQMATAPAVLQSLSLFLPAGTDETHDKDLPLOGEAPKLGPRPR-----YSFL 219
Db 205 LSLGAMVPALITVGSVLP-----DTPNSMIERGQHEEARHLKVRGVEDVDEFT 258
Qy 220 DLFRARDN-----MRGRTVGLGLVLFQOLTCQPNVLCYASTIFSSVGFH 264
Db 259 DLVHASEDSKVEHPWRNLLQKRYRPHLSMAIAIPFQOLTGINVMFYAPVLEDTIGF- 317
Qy 265 GSSAVLASVGLGAVKVAATITAMGLVDRAGRALLAGCALMALSVSGIGLVSAFVPM 324
Db 318 GSDAALMSAVITGLNVFATVSIYGVKWRRLFLLEGVOMLI----- 362
Qy 325 SGPSCLAVPNAT-----QOTGLPGDGLLDSSLPPIPTREDQREPISTAKTKPHPR 379
Db 363 ----CQAIVAACIGAKFGVCGAPGD----- 383
Qy 380 SGDSAPPRALSSALPCPPLPARGHALLRWT-----LLCLMVFSAFSEFGPVTWLVLS 436
Db 384 -----LPQYAVVVVLFICIYVSGFAMSGPLGWLVP 416
Qy 437 EIPVEIRGAFACFNSFMAANLP-----ISLSFLDLGTI--GLSWTFLYGLTAVLGL 490
Db 417 EIFPLEIRSA-----QSVNVSVNMFETTVVAAQVFLIMLCHKLFGI---FIFFSPVLIMS 469
Qy 491 GFYLFVPETKQSLAEIDQOFK 514
Db 470 IFVYFLPETKPIEENGQVWK 493

RESULT 11
ID GLCP_SYNY3 STANDARD; PRT; 468 AA.
AC P15729;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE GLUCOSE TRANSPORT PROTEIN.
GN GTR OR GLCP OR SLL0771.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90014182; PubMed=2507869;
RA Zhang C.-C., Durand M.C., Jeanjean R., Joset F.;
RT "Molecular and genetical analysis of the fructose-glucose transport system in the cyanobacterium Synechocystis PCC6803.";
RL Mol. Microbiol. 3:1221-1229(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91346660; PubMed=2129397;
RA Schmetterer G.R.;
RT "Sequence conservation among the glucose transporter from the cyanobacterium Synechocystis sp. PCC 6803 and mammalian glucose transporters.";
RL Plant Mol. Biol. 14:697-706(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Suglura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";

```

```

RL DNA Res. 2:153-166(1995).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements/ or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X15988; CAA34119.1; -
DR EMBL; X16472; CAA34492.1; -
DR EMBL; D64000; BAA10117.1; -
DR PIR; S06973; S06973.
DR PIR; S10014; S10014.
DR InterPro; IPR003663; Sugar_transport.
DR InterPro; IPR003662; sub_transport.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane; Transport; Sugar transport; Complete proteome.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 42 POTENTIAL.
FT DOMAIN 43 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 75 POTENTIAL.
FT DOMAIN 76 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 POTENTIAL.
FT DOMAIN 109 116 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 117 137 POTENTIAL.
FT DOMAIN 138 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 172 POTENTIAL.
FT DOMAIN 173 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 207 POTENTIAL.
FT DOMAIN 208 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 286 POTENTIAL.
FT DOMAIN 287 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 324 POTENTIAL.
FT DOMAIN 325 339 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 360 POTENTIAL.
FT DOMAIN 361 378 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 379 399 POTENTIAL.
FT DOMAIN 400 409 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 410 430 POTENTIAL.
FT DOMAIN 431 436 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 437 457 POTENTIAL.
FT DOMAIN 458 468 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 319 319 L -> I (IN REF. 1).
SQ SEQUENCE 468 AA; 49747 MW; D7EC345C4FB38D22 CRC64;

```

```

Query Match 16.8%; Score 464.5; DB 1: Length 468;
Best Local Similarity 26.3%; Pred. No. 4.4e-22;
Matches 141; Conservative 79; Mismatches 192; Indels 125; Gaps 12;

Qy 10 LCASVSLGLTFFGYELAVISGALLPLQLDFGLSCLEQEFVLGSLLLGALLASLVGGFLI 69
Db 19 LISGVAALGGFLPGFDTAVINGAVAAALQKHQTDLSLTGLSVSLALLGSLGAFGAGPIA 78
Qy 70 DCYGRKQAILGSLNVLVLAGSLTGLAGS-----LAWLVGRVAVGVFAISLSMACC 120
Db 79 DRHGRIK-----TMLAAVLEFTLSSIGSLPPTIWDFFIWRVLG---GIGVGAASVAP 129
Qy 121 IYVSELVGRGVLSVLEAGITVIGLLSVNAL-----AGTPW-----GWRHMF 168
Db 130 AYIAEVSPAHLRGLGSLQQLAIVSGIFIALLSNNFIALMAGGSAQNPLFGAAAARWRF 189
Qy 169 GWATAPAVLQSLSLFLP-----AGTDETHDKDLPLOGGEAPK-----LCP 211
Db 190 WTELIPALLYGVCAFLIPESPRYLVAQOGGEKAA--AILWKVEGGVDPSPRIEIQATVSLD 248

```


Matches	144;	Conservative	86;	Mismatches	175;	Indels	146;	Gaps	14;
QY	14	VSLGGLLTFGYELAVISGA	-----LLPLQLDFGLSCLEQBEFLVGLSLLGLGALLASLVG	65					
Db	16	VATIGGLLFGYDAVISGTVESLNTVFAPQNLSESAANSLGFCVASALIGCCIIGGALG	75						
QY	66	GFLIDCYGRKQAI--LGSNVLVLLAG	-----SLTLGLAGSLANLVLGRV	107					
		: : : :	: : : :						
Db	76	GYSNRFGRDRSLKIAAVLFFISGVSAWPELGFTSINPDNTVTVLAGYVPEFYIYRII	135						
QY	108	VGFAISLSNACCIIYVSELVCPRORGVLVSLYEAGITVGLLSYALNAYLA--CTPW--	162						
		: : : :	: : : :						
Db	136	GGTGVGLASLSPMYYIAELPAHIRGKLVSPNQFAITFGQLLVYCVNYFIARSGDASWLN	195						
QY	163	--GWRHFMFGNATAPAVLQSLSLFLP	-----AGTDETA-----THKDLIPLQGGEA	206					
Db	196	TDCWRYNEASECIPALLFLMLLYTVPESPRWLMSRGOEQAEIGILRIMGNTLATQAVQE	255						
QY	207	PK--LGPGRPRYSFLDLPRANDNRGRTTVGLGLVFOOLTQGQNVLCYASTIPSSVGFH	264						
Db	256	IKHSLDHCRKGTGRLLMFGV-----GVIVIGVMLSIFQQFVGINVLYIYAPEVKTLG-A	309						
QY	265	GGSSAVLASVGLGAVKVAATLTAMGLVDRAGRALLAGCALMALSYGIGLVSPFAVPM	324						
		: : : :	: : : :						
Db	310	STDIALLOTIIIVGINUTFTVLAINTVDKGRKPLQIIGALGMAGHPSLGTATPY-----	364						
QY	325	SGPSCLAVPNATGQTGLPGSGLLQDSSLPPIPRTNEDQREPIILSTAKTKPHPRSGDPS	384						
Db	365	-----TQAPG	-----	369					
QY	385	APPLALUSLGPPLPARGHALLRWNTALLCLAVFVSASFSGFGPVTVLWLSIYPVDIR	444						
		: : : :	: : : :						
Db	370	-----IVALLSMLEFYAAAFAMSWGVPVCVLLSEIFFPNAIR	404						
QY	445	GRAFAFCNSFNAAANLFLISLF--LD-----LIGTIGLSWTELLXGLTAVLGLGFIYLPV	498						
		: : : :	: : : :						
Db	405	GKALAIAYAQAQLTANYFVSWTFPMXDKNSLVAVHFHNGFSWIIYGCWCVLAALFMKKRVP	464						
QY	499	ETKGQSLAEID	509						
Db	465	ETRGKTLLEE	475						

RESULT 13

```

YFIG_BACSU      STANDARD;          PRT;      482 AA.
ID  AC          P54723;
DT  DT  01-OCT-1996 (Rel. 34, Created)
DT  DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  DE  HYPOTHETICAL METABOLITE TRANSPORT PROTEIN YFIG.
GN  GN  YFIG.
OS  OS  Bacillus subtilis.
OC  OC  Bacteria; Firmicutes; Bacillus/Clostridium group;
OC  OC  Bacillus/Staphylococcus group; Bacillus.
OX  OX  NCBI_TaxID=1423;
RN  RN  [1]
RP  RP  SEQUENCE FROM N. A.
RC  RC  STRAIN=168;
RX  RX  MEDLINE=96262713; PubMed=8704981;
RT  RT  Yamamoto H., Uchiyama S., Fajar A.N., Ogasawara N., Sekiguchi J.;
RT  RT  "Determination of a 12 kb nucleotide sequence around the 76 degrees
RT  RT  region of the Bacillus subtilis chromosome.";
RL  RL  Microbiology 142:1417-1421(1996).
CC  CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC  CC  -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC  CC  -----
CC  CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  CC  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC  CC  the European Bioinformatics Institute. There are no restrictions on its
CC  CC  use by non-profit institutions as long as its content is in no way
CC  CC  modified and this statement is not removed. Usage by and for commercial
CC  CC  entities requires a license agreement (see http://www.isb-sib.ch/announcement

```

```

CC or send an email to liscnee@lsb-slb.ch).
CC -----
CC ENBL; D50543; BAA09111.1; -.
CC EMBL; Z99108; CAB12655.1; -.
CC Subtilisin; BG11854; yfig.
DR InterPro; IPR003663; Sugar_trnsport.
DR InterPro; IPR003662; sub_transport.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRANSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Hypothetical protein; Transport; Membrane; Complete proteome.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 264 284 POTENTIAL.
FT TRANSMEM 302 322 POTENTIAL.
FT TRANSMEM 332 352 POTENTIAL.
FT TRANSMEM 353 373 POTENTIAL.
FT TRANSMEM 401 421 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
SQ SEQUENCE 482 AA; 52756 MW; 90851C4P4C48EE01 CRC64;

```

Query Match	16.48;	Score 452.5;	DB 1;	Length 482;
Best Local Similarity	25.09;	Pred. No. 2.5e-21;		
Matches 140; Conservative	89;	Mismatches .179;	Indels 151;	Gaps 14;

Qy	14	VSLGLGTFGYELAVISGALLPLQLDFG---LSCLEOBEFLVGSLLLGALLASLVGGGLID	70
Db	27	VSTFGGLLFYDGTGVINGA-LPFWATAGQLNLTPTVEGLVASSLLGNACFMFGRLSD	85
Qy	71	CYGRKQAIKSNLVLLAGSLTGLAGSLAWILGRAVVFSAISLMACCIVSELYSELVGP	130
Db	86	RHGRKKTILYLALFLFAATLCCTSPNASVMIAFRFLIGLAVGCASVTVPTELAISP	145
Qy	131	QRGVLSYIEAGITVGILLSYALNYALACTPWG-----WRMFGWATAPAVLOSLLFL	185
Db	146	RRGRIVTQNELMIWIGQLLAYTFN-AIIGTMGESANVMYMLVIATLPAYVLWFGMLIV	204
Qy	186	PAG-----TDETATH--KDILPLOGGEAPKLQ-----PGRPRY	216
Db	205	PESPRWLAAKRMGDALRYLRQIBEDSQAQQEIKEIKHAIEGTAKKAGFHDFQPWIRRI	264
Qy	217	SFDLFRARDNMGRITTVGLGLVFLFQOLTQOPNVLCYASTIFFSVGFHGSGASVLASVGL	276
Db	265	LF-----IGIGIAVQOITGVNSIMYYGTEILREAGFO-TEAALIGNIAN	308
Qy	277	GAVKVAATLTANGLDVRAGRRAILLAG--CALMALSVSGICLVSFVPMDSGPCSLAVPN	334
Db	309	GVISVIAVIFGIWLLGKVRRRPMLIIGOIGTMTALLLIGI-----	348
Qy	335	ATGOTGLPGDSLQLDSSLPIPTRNEDQREPILLSAKTKRPHRSGDPSPAPRLALSSA	394
Db	349	-----LSIV	352
Qy	395	LPGPPLPARGHALLRWHTALLCLMYPVSASFSGFGVPTMWLVISEIYVPBIRGRAFACNSP	454
Db	353	LEGTP-----ALPYVYVLSLTILFLAQFTAISTVTWMLSEIPFMHVRLGIMGISITFC	405
Qy	455	NWAANLISLSFLDLICTGITSWTFLLYGLTAVLGLGFIYLFVPTKGSLAEIDDOOFK	514
Db	406	LWTANLIGFTFPILLNNHIGMSATFFIFVANNNILAILEVKKYVPTPKGRSLQEHSHPQ	465
Qy	515	RRFTLSFGHR-----QNST	528
Db	466	-----YGRADQEIQNOT	478

RESULT 14

RESULT 14

```

ITR1_YEAST
ID ITR1_YEAST STANDARD; PRT; 584 AA.
AC P30605;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MYO-INOSITOL TRANSPORTER 1.
GN ITR1 OR YDR497C OR D9719.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250431; PubMed=2040626;.
RA Nikawa J.-I., Tsukagoshi Y., Yamashita S.;
RT *Isolation and characterization of two distinct myo-inositol
RT transporter genes of Saccharomyces cerevisiae.*;
RL J. Biol. Chem. 266:11184-11191(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkle-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yeiton M., Botstein D., Davis R.W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAJOR TRANSPORTER FOR MYO-INOSITOL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90352; BAA14366.1; -
DR EMBL; U33057; AAB64939.1; -
DR PIR; A40538; A40538.
DR SGD; S0002905; ITR1.
DR DR InterPro: IPR0033663; Sugar_trnsprt.
DR DR InterPro: IPR0033662; sub_trnsprt.
DR DR Pfam: PF00083; sugar_tr; 1.
DR DR PRINTS; PR00171; SUGTRNSPORT.
DR DR PROSITE; PS002116; SUGAR_TRANSPORT_1; 2.
DR DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane; Sugar transport; Glycoprotein.
FT TRANSMEM 87
FT TRANSMEM 107
FT DOMAIN 108 129
FT TRANSMEM 130 150
FT TRANSMEM 159 177
FT TRANSMEM 187 207
FT TRANSMEM 216 236
FT TRANSMEM 245 265
FT DOMAIN 266 337
FT TRANSMEM 338 358
FT TRANSMEM 373 393
FT TRANSMEM 404 426
FT TRANSMEM 446 467
FT TRANSMEM 480 500
FT TRANSMEM 509 529
FT DOMAIN 530 584
FT TRANSMEM 371 371
FT CARBOHYD
FT CONFLICT 43 44
FT SEQUENCE 584 AA; 63569 MW; 42543E30A102DC65 CRC64;

```

Query Match	15.8%;	Score 438;	DB 1;	Length 584;
Best Local Similarity	24.9%;	Pred. No. 2.5e-20;		

Matches 136; Conservative 85; Mismatches 218; Indels 108; Gaps 12;

QY 4 SPVPVLPKASVSLLGLTGYELAVISGALLPLQLDFGLSCL---EQEFLVGSLLLGALL 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 83 SPSFIITL-TPVASISGFMEFYDTGYISSALISIGTDHDKVLTGYEKERIVTAATSLGALI 141
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 61 ASLVGGFLIDCYGRKQAIIIGLSNLLIAGSLTLIAGSLAWLIWGVAVVGFSAISSMACC 120
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 142 TSIFAGTAADIFGRKKCLMGSNLMFVIGAILLOVSAAHTPMQMAVGLINGFGVGTCSLIAP 201
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 121 IYVSELVGPQRQRLVSVLYEAGITVGIILLSYALNTALAGTPTGWHRHFMGWATAPIVLQS 180
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 202 LFISEIAPKMRIGRUTVINSLMTGGQLVAYCGAGLNYYVNGWRILVGLSLIPTAQFT 261
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 181 SLFLP-----AGTDETATH-----KDLIPLOGGEAPKLGPGRP 214
| | | | | | | | | | | | | | | | | | | | | | | | | | | : | : | : | : | : | :
Db 262 CLCFLPDTPRYVMKGDLARAEVLKRSYTDTSSEIIBRKVEELVTLNQSPGNKVPEKV 321
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 215 RYSFDLFRARDNMGRRTVGLGVLFQOOLTCQPNNVICYASTIFFSVFHGGSSAVLASV 274
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 322 WNTIKELHTVPSNLRA-LIICGQIAIQOFTGWSLAFMVFSGTIPETVGF-KNSAV--SI 377
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 275 GLGAVKVAATLTAMGLVDPRAGRALLACG--ALMALSVSGIGLVSAVPMDSGPSCLAV 332
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 378 IVSGTNFTLVAFESIDKIRRIILLIGLPGMTMALVGCISIAHFUGIKFD-GAVAVV 436
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 333 PNATQOTGLPGDSLQQDSSLPIPTRNEDOREPILSTAKTKTRPHRSGDPSPAPRLALS 392
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 437 SSGFSWGIV-----STAKTKTRPHRSGDPSPAPRLALS----- 445
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 393 SALPGPPLPARGHALLRWTTALLCMVFSAFSGFGPVTWLVLSEIYPVEIRGRAFCW 452
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 446 -----VIIVFIVPAARYALGIGITVPW-QQSELPQNVRGIGTSYAT 486
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 453 SPNWAANFISLSFELDILIGTGLSWTELLXGLTAVLGIGFIYLFVPTKQSLAIEDQQF 512
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 487 ATNWAGSLVIASTFLTMLQNTIPAGTFAEFAGLSCLSTIFYCYFELSLELEV-QTI 545
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 513 QKRRTPL 519
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 546 LKDGFNI 552

RESULT 15
STA_RICCO
ID STA_RICCO STANDARD; PRT; 522 AA.
AC Q10710;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DB SUGAR CARRIER PROTEIN A.
GN STA.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
ON NCBI_TaxID=3988;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. CARMENCITA; TISSUE=Cotyledon;
RA Weig A., Franz J., Sauer N., Komor E.;
RT "Isolation of a family of cDNA-clones from Ricinus communis L.
RT with close homology to the hexose carriers.";
RL J. Plant Physiol. 143:178-183(1994).
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -! SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC

```
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08197; AAA79769.1; .
DR InterPro; IPR003663; Sugar_transport.
DR InterPro; IPR003662; sub_transport.
DR Pfam; PF00083; sugar_tr.1.
DR PRINTS; PR00171; SUGRTRANSPORT.
DR PRINTS; PR00172; GLUCTRNSPORT.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane; Transport; Sugar transport; Symport.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 144 164 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 351 371 POTENTIAL.
FT TRANSMEM 387 407 POTENTIAL.
FT TRANSMEM 427 447 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
SQ SEQUENCE 522 AA; 56873 MW; 327C0F186029A586 CRC64;

Query Match 15.6%; Score 430.5; DB 1; Length 522;
Best Local Similarity 25.5%; Pred. No. 6.4e-20;
Matches 145; Conservative 84; Mismatches 168; Indels 171; Gaps 18;

QY 14 VSLGLGTFGYELAVISGALLPLQLDFGLSCLEQEF----- 49
DB 33 VAAVGCSIFGYDIG-ISGVISMD-----AFLEKFFRSYVLYKKKHAHENNYCKYDDQRLA 86

QY 50 -LVGSLLLGALLASLVGGFLIDCYGRKQAIYGSNVLVLAGSLTLGLAGSLAWLVIGRAVV 108
DB 87 APTSSLYLAGLAASLVAGPITRIYGRRAIIISGGISFLIGAAINATINLAMLILGRIML 146

QY 109 GFAISLSSWACCIYVELVGPQRGVLYSLYEAGITVIGILLSYALNYALAGT----PWGW 164
DB 147 GVGIGFGNOAVPLYLSEMAPTHLRGGLNIMFQLATTSGIFTANMVNY---GTHKLESWGW 203

QY 165 RHMFCAWATAPAVLQSLSLFLP-----AGTDET-ATHKDLIPL 201
DB 204 RLSLGLAAAPALLWTIGLLLPETNSLIEQGLHEKGRNVLEKIRGTXHVDAEFODML-- 261

QY 202 QGGEAPKLGPCGRPRYSFLDLFRADNMGRRTVGLVLFOQLTQOPNVLCYASTIFSSV 261
DB 262 ---DASELA-NSIKHPFRNILEKRN--RPQLVMAIFMPTFQILTGINILFYAPPLFQSM 315

QY 262 GPHGSSAVLASVGLCAVKAATLTAMGLYDRAGRALLLAG-----CALMALSVSGIG 315
DB 316 GF-GGNAALYSSAVTGAVALCSSTFISIATVDRLGRFRLLISGGIOMITCOVIVAILGVK 374

QY 316 LVSEFVPMDSGSCLAVPNATGOTGLPGDSGLLDQSLSPPIPTNEDQREPILSTAKTK 375
DB 375 F-----GDNQQLSKS----- 384

QY 376 PHPRSGDPSAPPLRALSSALPGPLPARGHALLRWLTALICLMV--FVSASFSGFGPVTWL 433
DB 385 -----FSLVWVIMICLVLAFGWSGPLGWT 410

QY 434 VLSEIYPVEIRGPAFNSFNWAANLF-----ISLFDLDTIGTIGLSWTFLLYGLTAVLG 489
DB 411 VPSEIFPLETRAG---QSTITVAVNLFETVIAQSFPSLLCAKRFK-IFLFFAGWVTVM 465

QY 490 LCFIYLVFVETKQSLAEIDQOFQKRRF 517
DB 466 TAFVYIFLPETKGVPIEMIFLWRKWF 493
```

THIS PAGE BLANK (USPTO)